

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..324

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 31..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACATTCAGC TGACCCAGTC TCCANNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 60
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 120
NNNNNNNNNN NNCAGCCCTT GATTATGAG GTTCCAACC GGCCTCTGG AGTCCCAGAC 180
AGGTTCAGTG GCAGTGGGTC GGACACTGAT TTCACACTCA AAATCAGCAG AGTGGAGGCT 240
GAGGATGTTG GGGTTTATTA CTGCATGCAA TATACACACA TTCCATTCAC TTTCGGCCCC 300
GGGACCAAAC TGGATATCAA ACGA 324

B6
Feature

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Asp Ile Gln Leu Thr Gln Ser Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Pro Leu Ile
35 40 45
Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
50 55 60
Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
65 70 75 80
Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe
85 90 95
Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg
100 105

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

1 5 10 15 48
GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

20 25 30 96
GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGC AAT TAT
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr

35 40 45 144
TTA AAT TGG TAT CAA CAG AAA CCA GGG AAA GCC CCT CAG CCC TTG ATT
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile

50 55 60 192
TAT GAG GTT TCC AAC CGG GCC TCT GGA GTC CCA GAC AGG TTC AGT GGC
Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly

65 70 75 80 240
AGT GGG TCG GAC ACT GAT TTC ACA CTC AAA ATC AGC AGA GTG GAG GCT
Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala

85 90 95 288
GAG GAT GTT GGG GTT TAT TAC TGC ATG CAA TAT ACA CAC ATT CCA TTC
Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe

100 105 324
ACT TTC GGC CCC GGG ACC AAA CTG GAT ATC AAA CGA
Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile
35 40 45
Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
50 55 60
Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
65 70 75 80
Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe
85 90 95
Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg
100 105

(2) INFORMATION FOR SEQ ID NO:31

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

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Continue

GAC	ATT	CAG	CTG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	GCA	TCT	GTG	GGA	48
Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5					10					15		
GAC	ACA	GTC	ACC	ATC	ACT	TGT	CGG	GCA	AGT	CAG	GGC	ATT	AGC	AAT	AAT	96
Asp	Thr	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Ser	Asn	Asn	
			20					25					30			
TTA	GCC	TGG	TAT	CAG	CAG	AAA	CCA	GGA	AAA	GCT	CCT	AAG	CGC	CTG	ATC	144
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Arg	Leu	Ile	
		35					40					45				
TAT	GCT	GCA	TCC	AGT	TTG	GAA	AGT	GGG	GTC	CCA	TCA	AGG	TTC	AGT	GGC	192
Tyr	Ala	Ala	Ser	Ser	Leu	Glu	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	
	50					55					60					
AGT	GGA	TCT	GGG	ACA	GAA	TTC	ACT	CTC	ACC	ATC	AGC	AGC	CTG	CAG	CCT	240
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	
	65				70					75				80		
GAA	GAT	TTT	GCA	ACT	TAT	TAC	TGT	CAA	CAG	GAT	AAC	AGT	TAT	CCT	TTC	288
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Asp	Asn	Ser	Tyr	Pro	Phe	
				85					90					95		
ACT	TTC	GGC	GGA	GGG	ACC	AAG	GTG	GAG	ATC	AAA	CGA					324
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg					
			100					105								

(2) INFORMATION FOR SEQ ID NO:32

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Asn Ser Tyr Pro Phe
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

BC
Carter

(2) INFORMATION FOR SEQ ID NO:33

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

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Parker

GAC	ATT	CAG	CTG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	GCA	TCT	GTG	GGA	48
Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5					10					15		
GAC	ACA	GTC	ACC	ATC	ACT	TGT	CGG	GCA	AGT	CAG	GGC	ATT	AGC	AAT	AAT	96
Asp	Thr	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Ser	Asn	Asn	
			20					25					30			
TTA	GCC	TGG	TAT	CAG	CAG	AAA	CCA	GGA	AAA	GCT	CCT	AAG	CGC	CTG	ATC	144
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Arg	Leu	Ile	
		35					40					45				
TAT	GCT	GCA	TCC	AGT	TTG	GAA	AGT	GGG	GTC	CCA	TCA	AGG	TTC	AGT	GGC	192
Tyr	Ala	Ala	Ser	Ser	Leu	Glu	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	
	50					55				60						
AGT	GGA	TCT	GGG	ACA	GAA	TTC	ACT	CTC	ACC	ATC	AGC	AGC	CTG	CAG	CCT	240
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	
	65				70					75				80		
GAA	GAT	TTT	GCA	ACT	TAT	TAC	TGT	CAA	CAG	GAT	AAC	AGT	TAT	CCT	TTC	288
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Asp	Asn	Ser	Tyr	Pro	Phe	
				85				90						95		
ACT	TTC	GGC	GGA	GGG	ACC	AAG	GTG	GAG	ATC	AAA	CGA					324
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg					
			100					105								

(2) INFORMATION FOR SEQ ID NO:34

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Asn Ser Tyr Pro Phe
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

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Continue

GAC	ATT	GTG	ATG	ACT	CAG	TCT	CCA	ACT	TTC	CTT	GCT	GTG	ACA	GCA	AGT	48
Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Thr	Phe	Leu	Ala	Val	Thr	Ala	Ser	
1				5					10					15		
AAG	AAG	GTC	ACC	ATT	AGT	TGC	ACT	GCC	TCT	GAG	AGC	CTT	TAT	TCA	AGC	96
Lys	Lys	Val	Thr	Ile	Ser	Cys	Thr	Ala	Ser	Glu	Ser	Leu	Tyr	Ser	Ser	
		20					25					30				
AAA	CAC	AAG	GTG	CAC	TAC	TTG	GCT	TGG	TAC	CAG	AAG	AAA	CCA	GAG	CAA	144
Lys	His	Lys	Val	His	Tyr	Leu	Ala	Trp	Tyr	Gln	Lys	Lys	Pro	Glu	Gln	
		35				40					45					
TCT	CCT	AAA	CTG	CTG	ATA	TAC	GGG	GCA	TCC	AAC	CGA	TAC	ATT	GGG	GTC	192
Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Gly	Ala	Ser	Asn	Arg	Tyr	Ile	Gly	Val	
	50					55					60					
CCT	GAT	CGC	TTC	ACA	GGC	AGT	GGA	TCT	GGG	ACA	GAT	TTC	ACT	CTG	ACC	240
Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	
65					70					75				80		
ATC	AGC	AGT	GTA	CAG	GTT	GAA	GAC	CTC	ACA	CAT	TAT	TAC	TGT	GCA	CAG	288
Ile	Ser	Ser	Val	Gln	Val	Glu	Asp	Leu	Thr	His	Tyr	Tyr	Cys	Ala	Gln	
			85						90					95		
TTT	TAC	AGC	TAT	CCT	CTC	ACG	TTC	GGT	GCT	GGG	ACC	AAG	CTG	GAG	CTG	336
Phe	Tyr	Ser	Tyr	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	
			100					105					110			
AAA	CGG															342
Lys	Arg															

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Asp Ile Val Met Thr Gln Ser Pro Thr Phe Leu Ala Val Thr Ala Ser
1 5 10 15
Lys Lys Val Thr Ile Ser Cys Thr Ala Ser Glu Ser Leu Tyr Ser Ser
20 25 30
Lys His Lys Val His Tyr Leu Ala Trp Tyr Gln Lys Lys Pro Glu Gln
35 40 45
Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Ile Gly Val
50 55 60
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Ser Ser Val Gln Val Glu Asp Leu Thr His Tyr Tyr Cys Ala Gln
85 90 95
Phe Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
100 105 110
Lys Arg

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

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B
CDS

GCC	CTC	GTG	ATG	ACC	CAG	ACT	CCA	GCC	TCC	GTG	TCT	GCA	GCT	GTG	GGA	48
Ala	Leu	Val	Met	Thr	Gln	Thr	Pro	Ala	Ser	Val	Ser	Ala	Ala	Val	Gly	
1				5				10						15		
GGC	ACA	GTC	ACC	ATC	AAG	TGC	CAG	GCC	AGT	GAG	AAC	ATT	TAC	AGC	TCT	96
Gly	Thr	Val	Thr	Ile	Lys	Cys	Gln	Ala	Ser	Glu	Asn	Ile	Tyr	Ser	Ser	
			20					25					30			
TTA	GCC	TGG	TAT	CAG	CAG	AAA	CCA	GGG	CAG	CCT	CCC	AAG	CTC	CTG	ATC	144
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	
		35					40					45				
TAT	GGT	GCA	TCC	ACT	CTG	GCA	TCT	GGG	GTC	CCA	TCG	CGG	TTC	AAA	GGC	192
Tyr	Gly	Ala	Ser	Thr	Leu	Ala	Ser	Gly	Val	Pro	Ser	Arg	Phe	Lys	Gly	
	50					55					60					
AGT	AGA	TCT	GGG	ACA	GAG	TAC	ACT	CTC	ACC	ATC	AGC	GGC	GTG	CAG	CGT	240
Ser	Arg	Ser	Gly	Thr	Glu	Tyr	Thr	Leu	Thr	Ile	Ser	Gly	Val	Gln	Arg	
	65				70					75					80	
GAG	GAT	GCT	GCC	ACC	TAC	TAC	TGT	CTA	GGC	AGT	GAT	AGT	AGT	AGC	GAT	288
Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Leu	Gly	Ser	Asp	Ser	Ser	Ser	Asp	
				85				90						95		
ACT	GCT	TTC	GGC	GGA	GGG	ACC	GAG	CTG	GAG	ATC	CTA	TGT				327
Thr	Ala	Phe	Gly	Gly	Gly	Thr	Glu	Leu	Glu	Ile	Leu	Cys				
			100					105								

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ala Leu Val Met Thr Gln Thr Pro Ala Ser Val Ser Ala Ala Val Gly
1 5 10 15
Gly Thr Val Thr Ile Lys Cys Gln Ala Ser Glu Asn Ile Tyr Ser Ser
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
35 40 45
Tyr Gly Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys Gly
50 55 60
Ser Arg Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Gly Val Gln Arg
65 70 75 80
Glu Asp Ala Ala Thr Tyr Tyr Cys Leu Gly Ser Asp Ser Ser Ser Asp
85 90 95
Thr Ala Phe Gly Gly Gly Thr Glu Leu Glu Ile Leu Cys
100 105

Bp
Continue

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ACT GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG CAG 48
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15

TTG AAA TCT GGA ACT GCC TCT GTT GTG TGC CTG CTG AAT AAC TTC TAT 96
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
20 25 30

CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC CTC CAA TCG 144
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45

GGT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC AAG GAC AGC ACC 192
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60

TAC AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA GCA GAC TAC GAG AAA 240
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80

CAC AAA GTC TAC GCC TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC 288
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95

GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT TA 321
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ACT GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG CAG	48
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln	
1 5 10 15	
TTG AAA TCT GGA ACT GCC TCT GTT GTG TGC CTG CTG AAT AAC TTC TAT	96
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr	
20 25 30	
CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC CTC CAA TCG	144
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser	
35 40 45	
GGT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC AAG GAC AGC ACC	192
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr	
50 55 60	
TAC AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA GCA GAC TAC GAG AAA	240
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys	
65 70 75 80	
CAC AAA GTC TAC GCC TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC	288
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro	
85 90 95	
GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT TAG	321
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
100 105	

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

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C2

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
20 25 30

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCT GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAG GAT CAG	48
Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Glu Asp Gln	
1 5 10 15	
GTG AAA TCT GGA ACT GTC TCT GTT GTG TGC CTG CTG AAT AAC TTC TAT	96
Val Lys Ser Gly Thr Val Ser Val Val Cys Leu Leu Asn Asn Phe Tyr	
20 25 30	
CCC AGA GAG GCC AGC GTA AAG TGG AAG GTG GAT GGT GCC CTC AAA ACG	144
Pro Arg Glu Ala Ser Val Lys Trp Lys Val Asp Gly Ala Leu Lys Thr	
35 40 45	
GAT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC AAG GAC AAC ACC	192
Asp Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Asn Thr	
50 55 60	
TAC AGC CTG AGC AGC ACC CTG ACG CTG AGC AGC ACA GAC TAC CAG AGT	240
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Ser Thr Asp Tyr Gln Ser	
65 70 75 80	
CAC AAT GTC TAT GCC TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC	288
His Asn Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro	
85 90 95	
GTC ACC AAG AGC TTC AAC AGG GGA GAG TGT TAG	321
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
100 105	

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCT GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAG GAT CAG 48
Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Glu Asp Gln
1 5 10 15

GTG AAA TCT GGA ACT GTC TCT GTT GTG TGC CTG CTG AAT AAC TTC TAT 96
Val Lys Ser Gly Thr Val Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
20 25 30

CCC AGA GAG GCC AGC GTA AAG TGG AAG GTG GAT GGT GCC CTC AAA ACG 144
Pro Arg Glu Ala Ser Val Lys Trp Lys Val Asp Gly Ala Leu Lys Thr
35 40 45

GAT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC AAG GAC AAC ACC 192
Asp Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Asn Thr
50 55 60

TAC AGC CTG AGC AGC ACC CTG ACG CTG AGC AGC ACA GAC TAC CAG AGT 240
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Ser Thr Asp Tyr Gln Ser
65 70 75 80

CAC AAT GTC TAT GCC TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC 288
His Asn Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95

GTC ACC AAG AGC TTC AAC AGG GGA GAG TGT TA 321
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Glu Asp Gln
1 5 10 15
Val Lys Ser Gly Thr Val Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
20 25 30
Pro Arg Glu Ala Ser Val Lys Trp Lys Val Asp Gly Ala Leu Lys Thr
35 40 45
Asp Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Asn Thr
50 55 60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Ser Thr Asp Tyr Gln Ser
65 70 75 80
His Asn Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAT CCA ATT GCG CCT ACT GTC CTC CTC TTC CCA CCA TCT GCT GAT CAG	48
Asp Pro Ile Ala Pro Thr Val Leu Leu Phe Pro Pro Ser Ala Asp Gln	
1 5 10 15	
CTG ACA ACT GAA ACA GTC ACC ATC GTG TGC GTG GCA AAT AAA TTC CGT	96
Leu Thr Thr Glu Thr Val Thr Ile Val Cys Val Ala Asn Lys Phe Arg	
20 25 30	
CCC AAT GAC ATC ACC GTC ACC TGG AAG GTG GAT GAC GAA ATC CAA CAG	144
Pro Asn Asp Ile Thr Val Thr Trp Lys Val Asp Asp Glu Ile Gln Gln	
35 40 45	
AGC GGC TTC GAG AAC AGT ACA ACA CCG CAG AGC CCC GAG GAC TGT ACC	192
Ser Gly Phe Glu Asn Ser Thr Thr Pro Gln Ser Pro Glu Asp Cys Thr	
50 55 60	
TAC AAC CTC AGC AGC ACT CTG TCA CTG ACC AAA GCA CAG TAC AAC AGC	240
Tyr Asn Leu Ser Ser Thr Leu Ser Leu Thr Lys Ala Gln Tyr Asn Ser	
65 70 75 80	
CAC AGC GTG TAC ACC TGC GAG GTG GTC CAT CAC AAC TCG GGC TCA GCG	288
His Ser Val Tyr Thr Cys Glu Val Val His His Asn Ser Gly Ser Ala	
85 90 95	
ATC GTC CAG AGC TTC AAT AGG GGT GAC TGT TAG	321
Ile Val Gln Ser Phe Asn Arg Gly Asp Cys	
100 105	

544
C4

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

6
B
Original

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAT CCA ATT GCG CCT ACT GTC CTC CTC TTC CCA CCA TCT GCT GAT CAG	48
Asp Pro Ile Ala Pro Thr Val Leu Leu Phe Pro Pro Ser Ala Asp Gln	
1 5 10 15	
CTG ACA ACT GAA ACA GTC ACC ATC GTG TGC GTG GCA AAT AAA TTC CGT	96
Leu Thr Thr Glu Thr Val Thr Ile Val Cys Val Ala Asn Lys Phe Arg	
20 25 30	
CCC AAT GAC ATC ACC GTC ACC TGG AAG GTG GAT GAC GAA ATC CAA CAG	144
Pro Asn Asp Ile Thr Val Thr Trp Lys Val Asp Asp Glu Ile Gln Gln	
35 40 45	
AGC GGC TTC GAG AAC AGT ACA ACA CCG CAG AGC CCC GAG GAC TGT ACC	192
Ser Gly Phe Glu Asn Ser Thr Thr Pro Gln Ser Pro Glu Asp Cys Thr	
50 55 60	
TAC AAC CTC AGC AGC ACT CTG TCA CTG ACC AAA GCA CAG TAC AAC AGC	240
Tyr Asn Leu Ser Ser Thr Leu Ser Leu Thr Lys Ala Gln Tyr Asn Ser	
65 70 75 80	
CAC AGC GTG TAC ACC TGC GAG GTG GTC CAT CAC AAC TCG GGC TCA GCG	288
His Ser Val Tyr Thr Cys Glu Val Val His His Asn Ser Gly Ser Ala	
85 90 95	
ATC GTC CAG AGC TTC AAT AGG GGT GAC TGT TA	321
Ile Val Gln Ser Phe Asn Arg Gly Asp Cys	
100 105	

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Asp Pro Ile Ala Pro Thr Val Leu Leu Phe Pro Pro Ser Ala Asp Gln
1 5 10 15
Leu Thr Thr Glu Thr Val Thr Ile Val Cys Val Ala Asn Lys Phe Arg
20 25 30
Pro Asn Asp Ile Thr Val Thr Trp Lys Val Asp Asp Glu Ile Gln Gln
35 40 45
Ser Gly Phe Glu Asn Ser Thr Thr Pro Gln Ser Pro Glu Asp Cys Thr
50 55 60
Tyr Asn Leu Ser Ser Thr Leu Ser Leu Thr Lys Ala Gln Tyr Asn Ser
65 70 75 80
His Ser Val Tyr Thr Cys Glu Val Val His His Asn Ser Gly Ser Ala
85 90 95
Ile Val Gln Ser Phe Asn Arg Gly Asp Cys
100 105

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT GAG CAG 48
Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
1 5 10 15

TTA ACA TCT GGA GGT GCC TCA GTC GTG TGC TTC TTG AAC AAC TTC TAC 96
Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
20 25 30

CCC AAA GAC ATC AAT GTC AAG TGG AAG ATT GAT GGC AGT GAA CGA CAA 144
Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
35 40 45

AAT GGC GTC CTG AAC AGT TGG ACT GAT CAG GAC AGC AAA GAC AGC ACC 192
Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
50 55 60

TAC AGC ATG AGC AGC ACC CTC ACG TTG ACC AAG GAC GAG TAT GAA CGA 240
Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
65 70 75 80

CAT AAC AGC TAT ACC TGT GAG GCC ACT CAC AAG ACA TCA ACT TCA CCC 288
His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
85 90 95

ATT GTC AAG AGC TTC AAC AGG AAT GAG TGT TA 321
Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
100 105

C5
(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT GAG CAG	48
Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln	
1 5 10 15	
TTA ACA TCT GGA GGT GCC TCA GTC GTG TGC TTC TTG AAC AAC TTC TAC	96
Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr	
20 25 30	
CCC AAA GAC ATC AAT GTC AAG TGG AAG ATT GAT GGC AGT GAA CGA CAA	144
Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln	
35 40 45	
AAT GGC GTC CTG AAC AGT TGG ACT GAT CAG GAC AGC AAA GAC AGC ACC	192
Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr	
50 55 60	
TAC AGC ATG AGC AGC ACC CTC ACG TTG ACC AAG GAC GAG TAT GAA CGA	240
Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg	
65 70 75 80	
CAT AAC AGC TAT ACC TGT GAG GCC ACT CAC AAG ACA TCA ACT TCA CCC	288
His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro	
85 90 95	
ATT GTC AAG AGC TTC AAC AGG AAT GAG TGT TAG	321
Ile Val Lys Ser Phe Asn Arg Asn Glu Cys	
100 105	